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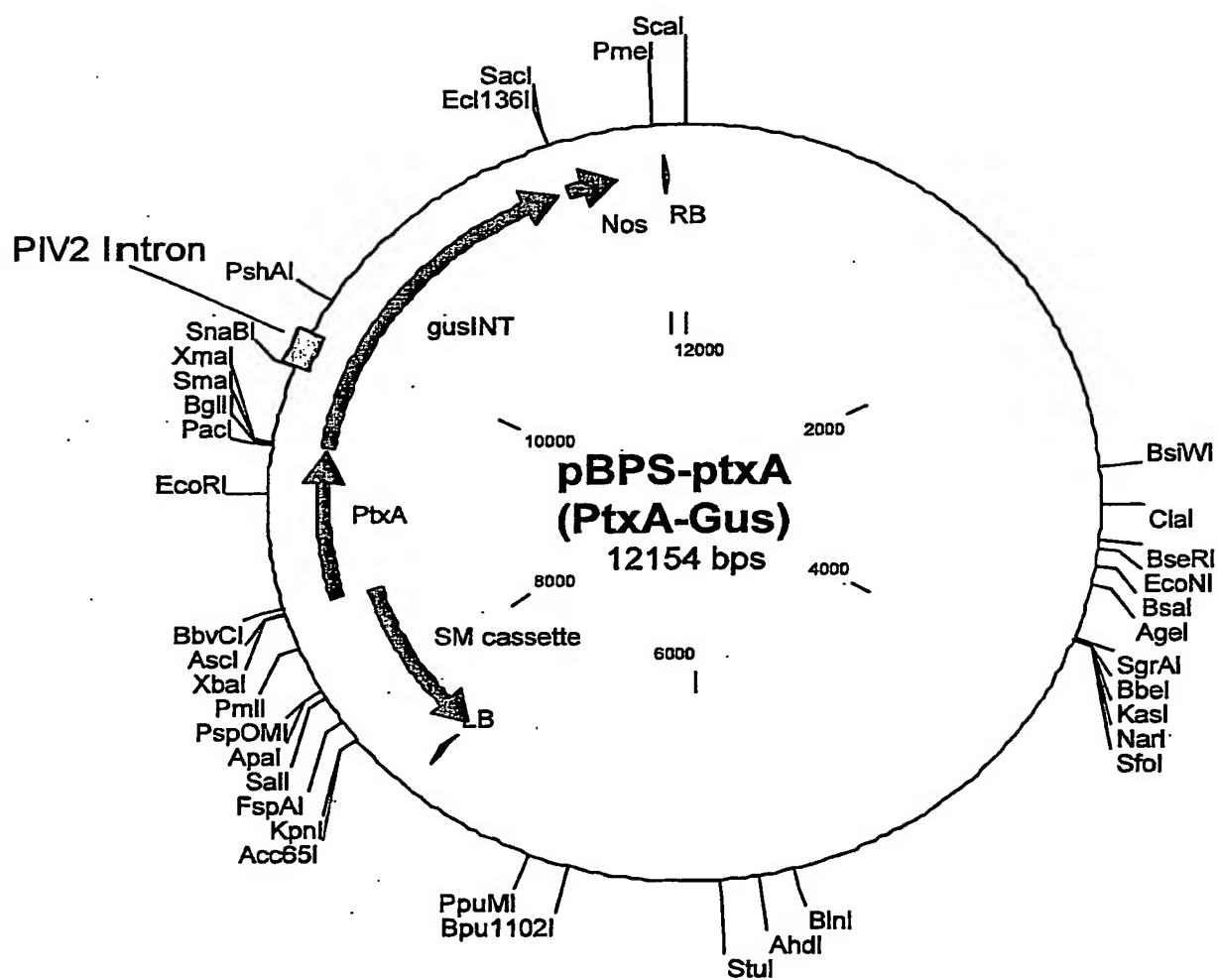


Fig. 1

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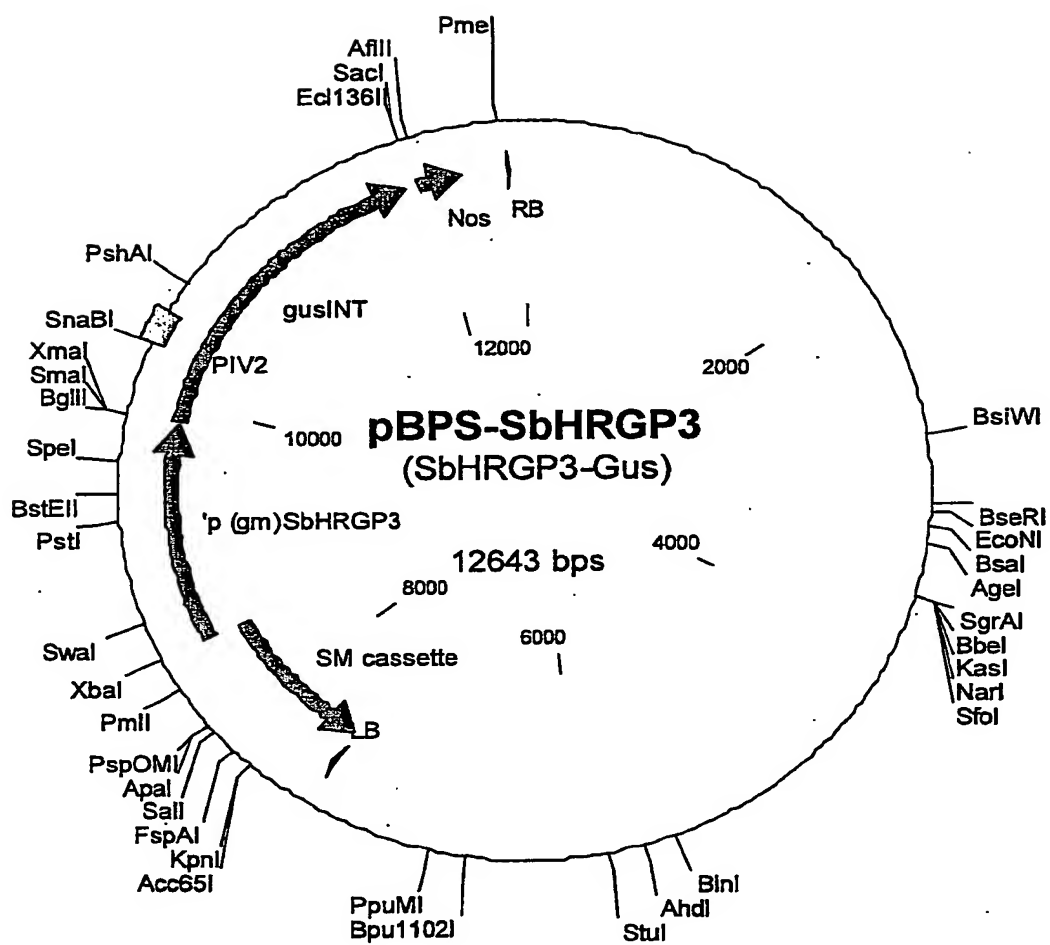


Fig. 2

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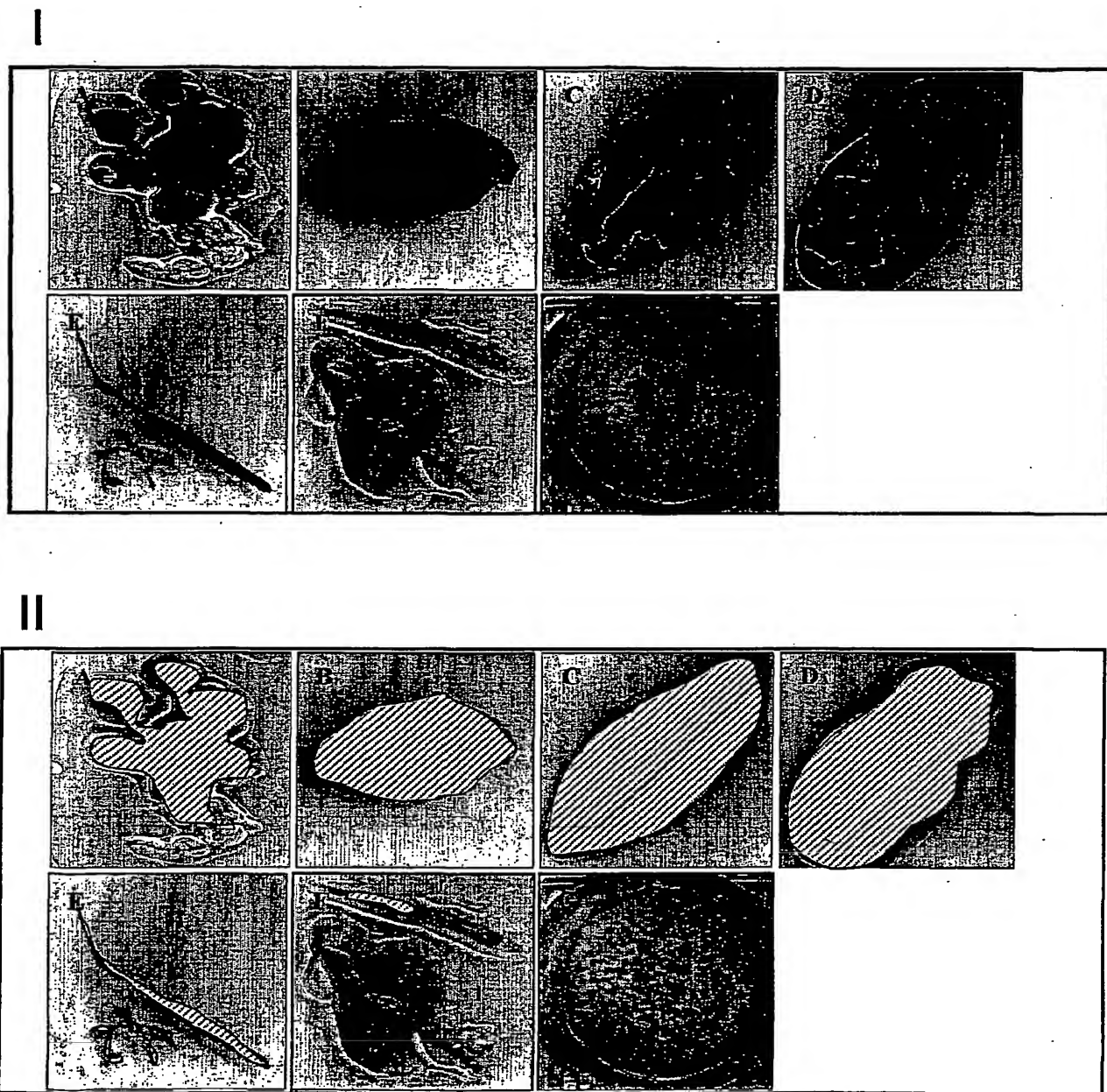


Fig 3

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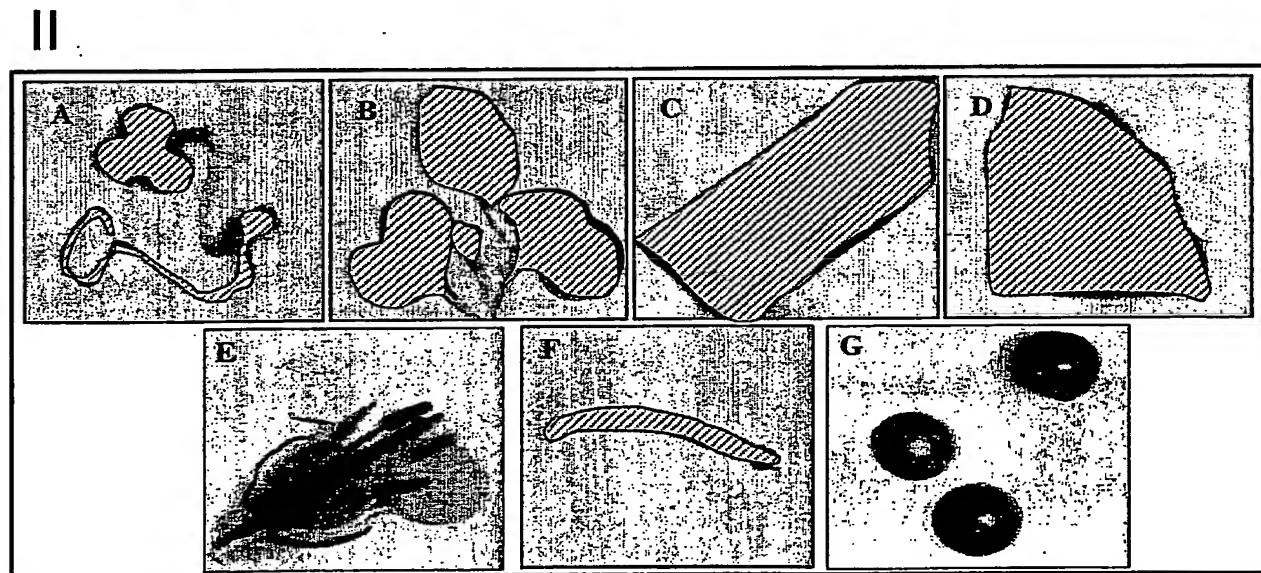
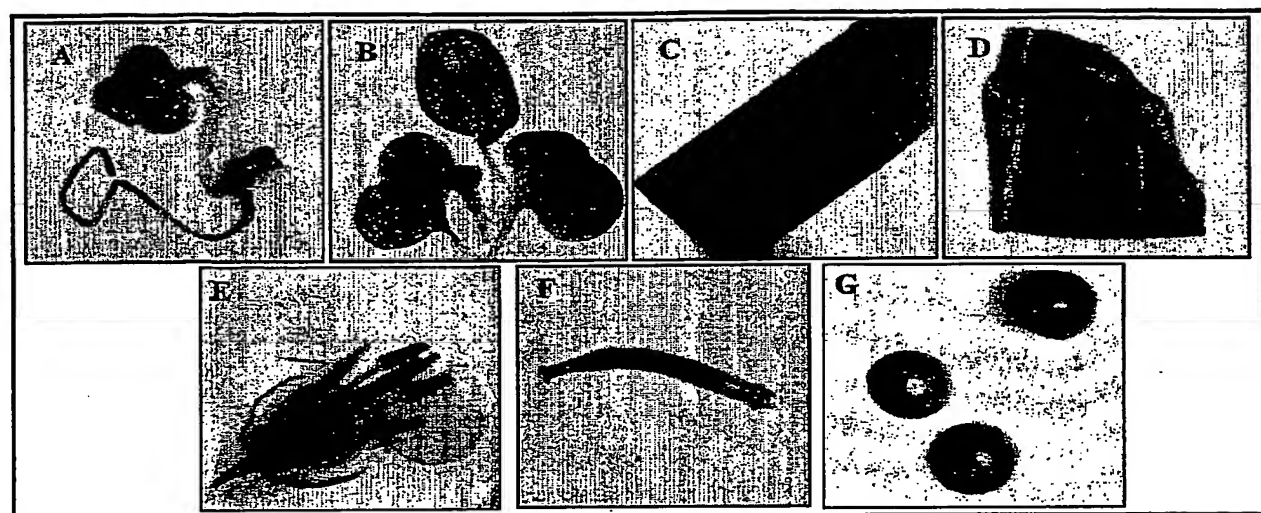


Fig 4

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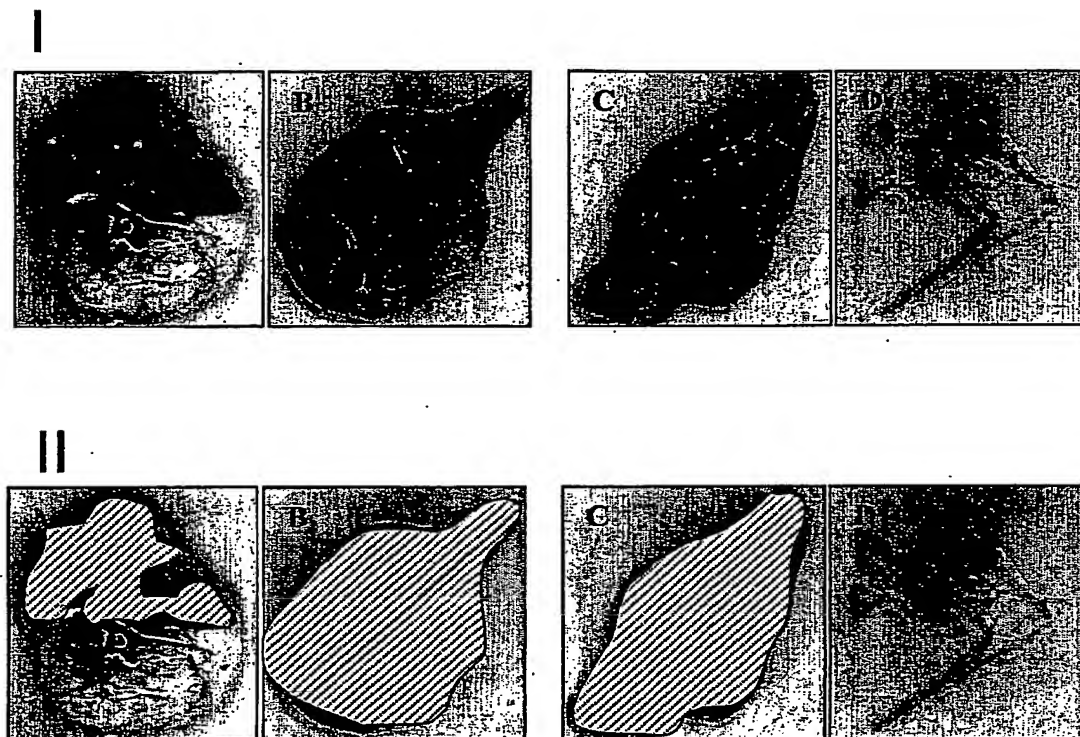


Fig 5

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	1	50
A	(1) MANFAIANVLILLLNSTLLNVLACPYCPYSPKPPTHKPPIVKPPVHK-	
B	(1) MANYALANVFILLLNSTLLIVLACPYCPYSPKPPTHHPPIVKPPVHKR	
C	(1) -----	
D	(1) -PHVKPPSTPKHPKDPHVKPPSTPKQPPYVKPPTTPKHPPHVKPPS---	
E	(1) MGKHGLATWLVILLNFATLLTSLACSYCPSPSP-----	
F	(1) MGSRLASFFVFLIFTVITLPTTIQACTPCTRPHPFVKP-----	
Consensus	(1) MA ALAS ILLLN STLL LAC YCPYSP PP PP VKPP	
	51	100
A	(50) -----PPKQPCPPSSSPKPPHVKPPHYKPPAVHP	
B	(51) RKYSPTPKPPVHKPPRYPPKSPCPPSSSTPKPPHVKPPHHKPPVVP	
C	(1) -----RAESART	
D	(47) -----TPKHPPKHP-----QKPCPPSSHGPKPPIVKPP	
E	(35) -----KPP-----KVKHPLPLPPKHPPHVKPP	
F	(41) -----PQHGGGGGGGSKPPPHGGGKGGGKPP	
Consensus	(51) PK PP K PH PPP H PKPP VKP	
	101	150
A	(83) PHVVKPP-AVHPPHVKPPVVPVHPPIVHPPYVKP-----PPVVKPP-----	
B	(101) PHVVKP--PVHPPYVKPPIVKPPIVHPPYVKP-----PPVVKPPYVKP	
C	(8) HHMFQP--HPP-YVKPPIVKPPIVHPPYVKP-----PPVVKPP-----	
D	(75) PHVPRPP-IVHPPIVSPPSTPKPPKTPPTTPKPPSPPIPIVSPP-----	
E	(57) PHTMP-----PNPPAVKPPYVKP-----PPVVEPP-----	
F	(67) PHGGKGGGPPHHGGGGGGGGKSPVVRPPPVVVRP--PPIIRPP-----	
Consensus	(101) PHVVKP VHPYVKPPIV PPIVHPPYVK PPVVKPP	
	151	200
A	(122) --VVKPPHVKPPVVPVTPPYIPKPPIVFPFHVLPP--VVPVTPPYVKP	
B	(144) PPVVRPPYVKPPVVPVTPPYVKPPVVRPPYVKPP--VVPVTPPYVKP	
C	(44) -----PYVKPPVVRPPYVKPP--VVPVTPPYVLS	
D	(119) -----IVYPPITPTPIVHPPVTPKPPSPTPIIVSPPIVY	
E	(83) -----YVKPPVVKPPYVKP-----PVVEPPYMP	
F	(109) -----PVYPPPIVRPPPIITRPPIIIPPIQPPVTT	
Consensus	(151) V PPYVKPPIVRPPYVKPP VVPVTPPYVL	
	201	250
A	(168) P-----PIVFPPHVLPVVPVTPPYVP-----KPPIVFPFHVLPPVVP	
B	(192) PPIVKPPIVFPPHVLPVVPSPPPYVSPPIVKPPIVFPPHVLPVVP	
C	(73) HHCFFP-TTVSTSSCTITTTLCTNTPIVN-----HQLFFHHMFFYLPVVP	
D	(154) PPITPTPVVSPPIIPTPIIVSPPFVFN-----PPVV	
E	(108) -----	
F	(140) PPGLLPPIITPPG--LLPPVTTTPGLLP-----PVTTPPG	
Consensus	(201) PP PIV PP V L P V SPPIVP I F PL PVVP	
	251	300
A	(208) VTPPYVLPVVPVTPPFVTPPIITPPTPTVFPVSPSPSETPCPPPPPTV	
B	(242) VTPPYVQPP--PIVTPPTPTPIVTPPVVSPPTP--PSETPCPPPLVP	
C	(116) VTPPYVQPT-----TYCNSTNTNTSNWTPPTP--PSETLVLPPLVP	
D	(186) IPPPYVSP-----PVVTPPIVTPPTPCPP-----PPPPAI	
E	(108) -----H	
F	(173) LLPPIINFP-----PVTVPPSSGYPPYG-----PPSGG	
Consensus	(251) VTPPYVQPP P IV PP TPPTP PSET PPPP	

Fig. 6a

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	301	350
A	(258)	VPYPPPAQPTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD
B	(287)	YPPTPPAQQTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD
C	(156)	YP-PPPAQQTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD
D	(219)	IP-SPPAQPTCPIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD
E	(109)	DT-----L---KLGACVDLLGGLVHIGIGSSAKDTCCPVLQGLVD
F	(202)	GGGGGGKQPTCPINALKLGACVDVLGGLIHIGLGNPVENVCCPVLQGLLE
Consensus	(301)	P PPAQPTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD

	351	397
A	(308)	LDAAVCLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPSS-
B	(337)	LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAY-
C	(205)	LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAS-
D	(268)	LDAAICLCTTIRLKLLNINIILPIALQVLIDDCGKYPPKDFKCPST-
E	(146)	LDAAVCLCTAIKVKLLNVNIIIPIALQVLVG-CGKTPPSGFQCPA--
F	(252)	LEAAVCLCTTIRLKLLNINIFIPLALQALIT-CGINPPSGFVCPPLT
Consensus	(351)	LDAAICLCTTIRLKLLNINIVIPALQVLID CGKTPPEGFKCPAS

Fig. 6b

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	551	600
B	(551) AAAAAC TAAAAAATAATTTCTCTCCTGATTTATATGAAATGACATTTTTT	
A	(1) -----CGCAATTTTTT	
Consensus	(551) G ATTTTTT	
	601	650
B	(601) TGGAACTGAAGG-GTATTGATTTTTACCACCTTTTACACCT--TTCAAA	
A	(12) GTGAAGCTGAGGGAGGATTGGATTTTTACACCTATTCAAAAGTCATTCAAA	
Consensus	(601) GAA TGA GG G ATTG TTTTAC C TT A A T TTCAAA	
	651	700
B	(648) G-----CCATTCAAGGATGAATATAGATTTTTTGGGCGATCAAACAC	
A	(62) GTTGTCCCTCCATTCAAGGATGAATGTAGATTTTTCAAGCATCAAACAC	
Consensus	(651) G CCATTCAAGGATGAAT TAGATTTTT ATCAAACAC	
	701	750
B	(689) AAGAATCATTACGATAACATGCTTTGGAACACACACATGCTTAAATTAAT	
A	(112) AAGAATCACTAGCATAACATGCTTTGAAACCCACACA--CTTAAATTAAT	
Consensus	(701) AAGAATCA TA ATAACATGCTTTG AAC CACACA CTTAAATTAAT	
	751	800
B	(739) GGTGGAGTATCAAAT----TTTAAAAT-ATTGTTGTCAAT-ACATACCC	
A	(160) GTTAGGAATATCAAATCCAATATAAAATCATAGTTGTCAATTACATACTC	
Consensus	(751) G T GGA TATCAAAT T TAAAAT AT GTTGTCAAT ACATAC C	
	801	850
B	(783) CGTCAATCTTCTTTTTTTTACCCAATAAACATTGAAATGTTGCTTCTTTC	
A	(210) AATCAAGTCCCTTTCTTTTACCCAATAAACATCAACATATTGCTTCTTCC	
Consensus	(801) TCAA CTTT TTTTACCCAATAAACAT A AT TTGCTTCT C	
	851	900
B	(833) GTTAAGCATAAAACATCAAAGTCTA-----GCAAAATGTTGTTTTTGC	
A	(260) ATTAAGCATATAAACATCAAAGTCTAAAGCTAGCAAAATGTTGTTTTTAG	
Consensus	(851) TTAAGCATA AAACATCAAAGTCTA GCAAAATGTTGTTTTT	
	901	950
B	(877) GATGACACATTTTCATA--TAGTTTAAAGGATGCATGATTTCGATTACAAAA	
A	(310) GATGACACATTTTCATACATAGTTTAAAGATACTTGATTTCGATTACAAAA	
Consensus	(901) GATGACACATTTTCATA TAGTTTAAA GAT C TGATTTCGATTACAAAA	
	951	1000
B	(925) ACAAATACTAATAATTCTAGCACAAAGTTTAAAGCAAGATTATAAAGCT	
A	(360) AGAAATTACCAATAGTT-TAGCACAAAGTCTAAAGCATAATTA--AAGCA	
Consensus	(951) A AAA TAC AATA TT TAGCACAAAGT TAAAGCA ATTA AAGC	
	1001	1050
B	(975) TCATAGCATGTGGATATTCATTTAGAAATATAGATTA-GATTGCCCTTTT	
A	(407) TCA---CATGTGCAGATTTAT---GAAAAAAGATTAAAGATTGCCCTTTT	
Consensus	(1001) TCA CATGTG A ATT AT GAAA A AGATTA GATTGCCCTTTT	
	1051	1100
B	(1024) CATCACGGGTC---TAACAGCACCCTTGTCCTACTACATGTCAAAAA--TG	
A	(451) CATCACGGGTCGAATAATAGCACTACTTGTCCTACTACATGTAAAAAATG	
Consensus	(1051) CATCACGGGTC TAA AGCAC ACTTGTCCTACTACATGT AAAA TG	
	1101	1150
B	(1069) TCCTCTAGTACAGCACCGCTTTTTTACTTGATTCCCCTTGTCATGCATGA	
A	(501) TCCTCTAGTACATCAAACTTTTTCCATTGATTCCCCTTATCC----ATGA	
Consensus	(1101) TCCTCTAGTACA CA TTTT TTGATTCCCCTT TCC ATGA	
	1151	1200
B	(1119) AAAAAATCAAAACAATATTTGGACACACAAACTTGCCCCCACTTTCCTTT	
A	(547) AAAAAATAAACAAATTCTTAAGACACAAAAAATGGCCCCACAT-CCTTT	
Consensus	(1151) AAAAAAT AA A A T TT GACACA AAA TG CCCCAC T CCTTT	

Fig. 7a

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		1201		1250
B	(1169)	TTCTTTCTGCCCTAGTTTGTGTTGAGACTCATATTGATCAAATTTGGCTAT		
A	(596)	---TTTCTGGCCTAGTTTGTGTTGA-----		
Consensus	(1201)	TTTCTG CCTAGTTTGTGTTGA		
		1251		1300
B	(1219)	GAATTCAAACAAAAAATTCACCTCTACCCATTGCATGTGT---GGGGCCCA		
A	(617)	-----A-----TTCATTCTAACTCTTGAATATGTAACGAGGCCCA		
Consensus	(1251)	A TTCA TCTA C TTG AT TGT G GGCCCA		
		1301		1350
B	(1266)	CATATAAATCCATGAAGGATTTCAATGTCCATCCAAGTCAATGATTCAAC		
A	(652)	C-TAAAAATCAAT-----CAATGATTAAAC		
Consensus	(1301)	C TA AAATC AT CAATGATT AAC		
		1351		1400
B	(1316)	ATATATAACATTGAATAATTTAATTCCAATTTGCAGTATTATGATTTAGA		
A	(676)	ATAAAAAA---TGAATAGTTTAATTCCAATTTGC-----		
Consensus	(1351)	ATA A AA TGAATA TTTAATTCCAATTTGC		
		1401		1450
B	(1366)	TTGATTGCTGCAATACGGTCCGTGAATGTGATCACTCACGAGAAAGAGGT		
A	(707)	-----TGCAACATGGTCCGTGAATATGA---CTCACGAGAAAGATAT		
Consensus	(1401)	TGCAA A GGTCCGTGAAT TGA CTCACGAGAAAGA T		
		1451		1500
B	(1416)	ATCAAAATTTCAAGGTATTTTATTTATTTTAAACAAATAAAATTTCAAGG		
A	(746)	ATCAAAATATCAA-----AATTTTCATAG		
Consensus	(1451)	ATCAAAAT TCAA AATTTCA G		
		1501		1550
B	(1466)	TCTTGTTTACCATATAAACCTCCTCACTCACACCCAATTCTCTTAAGTGT		
A	(769)	TTTTTTTACCATATAAACCTCATCACTCATTC--TATTTTTTTAAGTGC		
Consensus	(1501)	T TT TTCACCATATAAACCTC TCACTCA C ATT T TTAAGTG		
		1551		1600
B	(1516)	ATGACTTCATAGTAC--ACTACACTACTTTCTTTGAAACATGGCTAACTA		
A	(817)	AAAGCTTCATAGTAGTGAGCACACACATTACACTAAAATCTTCGAAACTT		
Consensus	(1551)	A CTTCATAGTA A ACAC TT C T AAA T AACT		
		1601		1650
B	(1564)	TGCTCTAGCCAATGTTTTTCATCCTTCTCTTGAACCTTGAGTACCTTACTCA		
A	(867)	A-----		
Consensus	(1601)			

Fig. 7b

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1 50

SEQ ID NO: 9 (1) ---CTTTTCAACAATCATGCCCATGTCAAGTGTAACAGGTTTACCTCT
 SEQ ID NO: 8 (1) AAGCTTTTCAACAATCATGCCCATGTCAAGTGTAACAGGTTTACCTCT
 SEQ ID NO: 7 (1) AAGCTTTTCAACAATCATGCCCATGTCAAGTGTAACAGGTTTACCTCT
 Consensus (1) AAGCTTTTCAACAATCATGCCCATGTCAAGTGTAACAGGTTTACCTCT
 51 100

SEQ ID NO: 9 (48) CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
 SEQ ID NO: 8 (51) CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
 SEQ ID NO: 7 (51) CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
 Consensus (51) CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
 101 150

SEQ ID NO: 9 (98) TTACATAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA
 SEQ ID NO: 8 (101) TTACATAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA
 SEQ ID NO: 7 (101) TTACATAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA
 Consensus (101) TTACATAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA
 151 200

SEQ ID NO: 9 (148) AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
 SEQ ID NO: 8 (151) AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
 SEQ ID NO: 7 (151) AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
 Consensus (151) AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
 201 250

SEQ ID NO: 9 (198) TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
 SEQ ID NO: 8 (201) TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
 SEQ ID NO: 7 (201) TTCAGTTAAGATTTAAATAGTATAA-TTAAAAATTATCGATGATGACAAA
 Consensus (201) TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
 251 300

SEQ ID NO: 9 (248) AAATTGTAAATATAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
 SEQ ID NO: 8 (251) AAATTGTAAATATAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
 SEQ ID NO: 7 (250) AAATTGTAAATATAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
 Consensus (251) AAATTGTAAATATAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
 301 350

SEQ ID NO: 9 (298) AATATCGAGAAAAAATATGTGATTATATATATGTGTGAGCTGAGTGAA
 SEQ ID NO: 8 (301) AATATCGAGAAAAAATATGTGATTATATATATGTGTGAGCTGAGTGAA
 SEQ ID NO: 7 (300) AATATCGAGAAAAAATATGTGATTATATATATGTGTGAGCTGAGTGAA
 Consensus (301) AATATCGAGAAAAAATATGTGATTATATATATGTGTGAGCTGAGTGAA
 351 400

SEQ ID NO: 9 (348) TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA
 SEQ ID NO: 8 (351) TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA
 SEQ ID NO: 7 (350) TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA
 Consensus (351) TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA
 401 450

SEQ ID NO: 9 (398) ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG
 SEQ ID NO: 8 (401) ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG
 SEQ ID NO: 7 (400) ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG
 Consensus (401) ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG
 451 500

SEQ ID NO: 9 (448) TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG
 SEQ ID NO: 8 (451) TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG
 SEQ ID NO: 7 (450) TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG
 Consensus (451) TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG
 501 550

Fig. 8a

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SEQ ID NO: 9(498) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
SEQ ID NO: 8(501) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
SEQ ID NO: 7(500) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
Consensus      (501) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTAAATTATGTA
                    551                                     600

SEQ ID NO: 9(548) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
SEQ ID NO: 8(551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
SEQ ID NO: 7(550) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
Consensus      (551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
                    601                                     650

SEQ ID NO: 9(598) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
SEQ ID NO: 8(601) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
SEQ ID NO: 7(600) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
Consensus      (601) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
                    651                                     700

SEQ ID NO: 9(648) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAA-----
SEQ ID NO: 8(651) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAA-----
SEQ ID NO: 7(650) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAAAGCAAAA
Consensus      (651) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAA
                    701                                     750

SEQ ID NO: 9(692) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
SEQ ID NO: 8(695) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
SEQ ID NO: 7(700) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
Consensus      (701) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
                    751                                     800

SEQ ID NO: 9(742) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
SEQ ID NO: 8(745) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
SEQ ID NO: 7(750) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
Consensus      (751) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
                    801                                     850

SEQ ID NO: 9(792) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
SEQ ID NO: 8(795) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
SEQ ID NO: 7(800) TGCAATATGCACATATTCGTTTTAGGCTTTTAGC-TCCACGATCTGTTAA
Consensus      (801) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
                    851                                     900

SEQ ID NO: 9(842) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
SEQ ID NO: 8(845) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
SEQ ID NO: 7(849) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
Consensus      (851) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
                    901                                     950

SEQ ID NO: 9(892) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTCACCATGCATAA
SEQ ID NO: 8(895) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTCACCATGCATAA
SEQ ID NO: 7(899) CAGGGAAGCACTAGAAGATATGAAATGAC-TAAAAGGTCACCATGCATAA
Consensus      (901) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAGGTCACCATGCATAA
                    951                                     1000

SEQ ID NO: 9(942) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
SEQ ID NO: 8(945) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
SEQ ID NO: 7(948) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
Consensus      (951) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT

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Fig. 8b

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1001
SEQ ID NO: 9(992) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
SEQ ID NO: 8(995) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
SEQ ID NO: 7(998) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
Consensus (1001) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
1050
1051
SEQ ID NO: 9(1042) TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
SEQ ID NO: 8(1045) TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
SEQ ID NO: 7(1048) TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
Consensus (1051) TTTATTTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
1100
1101
SEQ ID NO: 9(1092) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
SEQ ID NO: 8(1095) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
SEQ ID NO: 7(1098) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
Consensus (1101) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
1150
1151
SEQ ID NO: 9(1142) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCACAA
SEQ ID NO: 8(1145) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCACAA
SEQ ID NO: 7(1148) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCACAA
Consensus (1151) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCACAA
1200
1201
SEQ ID NO: 9(1192) CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
SEQ ID NO: 8(1195) CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
SEQ ID NO: 7(1198) CCAACTTGGT-----CCAAAAAACTCAATATCAATATTTTCGAAAT
Consensus (1201) CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
1250
1251
SEQ ID NO: 9(1242) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
SEQ ID NO: 8(1245) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
SEQ ID NO: 7(1239) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
Consensus (1251) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
1300
1301
SEQ ID NO: 9(1292) TCCACCTACCAAGATAAAATAGTTGGATAAAATGGGTAAAAAAAGTTGTAT
SEQ ID NO: 8(1295) TCCACCTACCAAGATAAAATAGTTGGATAAAATGGGTAAAAAAAGTTGTAT
SEQ ID NO: 7(1289) TCCACCTACCAAGATAAAATAGTTGGATAAAATGGGTAAAAAA-GTTGTAT
Consensus (1301) TCCACCTACCAAGATAAAATAGTTGGATAAAATGGGTAAAAAAAGTTGTAT
1350
1351
SEQ ID NO: 9(1342) AAAGGGCAACACTACCTCTCCTAATGGCAGTA-----
SEQ ID NO: 8(1345) AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAACCCAAG
SEQ ID NO: 7(1338) AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAACCCAAG
Consensus (1351) AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAACCCAAG
1393

```

Fig. 8c

13/13

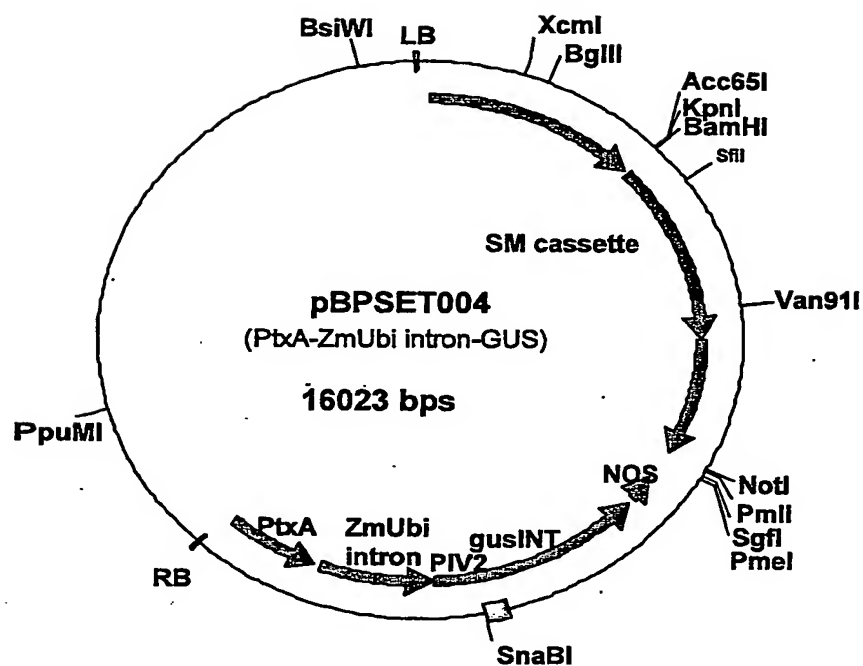


Fig. 9